

Sequence Name	Description	Length	Score	Opt. Frame
1. hnu31875	TOIG of: hnu31875	292	1442	412 621 0.00 0
1. US-10-033-223-1 (1-1283)	check: 2920	From: 1	to: 1442	
Initial Score =	412	Optimized Score =	621	Significance = 0.00
Residue Identity =	618	Matches =	642	Mismatches = 372
Gaps =	23	Conservative Substitutions =	0	
CACCAAGCGTGAGACTATACCTATCCGCAAGTGGCTGTAGTTACAGAGAAAGCATCTCAGACCAACAC				
370 380 390 400 410 420 430				
GCTGTGTGATTCATGCAACAGCGCGGGGTGCTAGAGCCCTGTGCCCCGGCTTGGAAATTCGGTGGGATG				
30 40 50 60 70 80 90				
TATGCTGTACAGATGTGCGCGGGCTACCAAGAGCTGTTCATCCCTGTGCTAGAGCTTTCTGTGAGATAG				
440 450 460 470 480 490 500				
100 110 120 130 140 150 160				
CAGCTTCGGGATGACCCCGCGGAGCCCGCTCCGAATAATAGTGGCCCTGTAAAGCCCTCCACCGGAT				
510 520 530 540 550 560 570				
CAGCACCGGAGATGACAGAGAGGCGCTCTGTGTAACCGGATAGCCGTGTCAACCGGGTCCACAGTGGAT				
170 180 190 200 210 220 230				
CGGCTTCGCATGCGCCCGCGCTTTGGAGCCCAAGACCGGGGCCCATTTGATGTCTCAGACACCGGAGCAG				
580 590 600 610 620 630 640				
CGGCTTCGCATGCGCCCGCGCTTTGGAGCCCAAGACCGGGGCCCATTTGATGTCTCAGACACCGGAGCAG				
650 660 670 680 690 700 710 720				
CGTGGACCGGGCCATGCGCCAGCTGTCAGAGGGGAGGGGCTGAGTGTGCGGACATTTGTCTCCACGTGGGA				
320 330 340 350 360 370 380				
GGCGAGAGACCGGAGAGCGGGTGTGTGTCACAGGCTGTGAAGCTTCATAGAGGTATCATATCTAGTCTCAA				
730 740 750 760 770 780 790				
GGCTGAGGACCGGAGACGCTGTGTGTCACAGGCTGTGAAGCTTCATAGAGGTATCATATCTAGTCTCAA				
390 400 410 420 430 440 450				
TGCTGCTGTCAACCCCTTTCTTTGGAAACATATAGATGTCTCATGAGAGGCTGTGGAGCAAGACTTGACAT				
800 810 820 830 840 850 860				
CGCAGGGGTCAACCTCTGTGAGAGGACTCTGAGGACCAAGTACAGATCTGGAGCAAGATCTTAAGTGT				
460 470 480 490 500 510 520				
TAATGTAGAGGCCCCAGGCTTGTATGACCAAGAGCGAGTGTGCCAAGAAATAGAGAAACAGAGGCGGCTCA				
870 880 890 900 910 920 930				
GAACTGTAAGTCCCAAGCCCTGTGCTAGGCAAGTGTGCTGCCTACATAGAGAAAGAGAGGGGTGCTGT				
530 540 550 560 570 580 590				
GGTATGCTGTCTTCTTCATAGAGAGCTTCAAGTTCATCTCTGGCTTCAAGTCTTTACAAATGTCAATAAAC				
940 950 960 970 980 990 1000				
CATCTGTATCTTCTTCATAGAGAGCTTAAATACAGTATGAGCGCTGGGTGTCTAATAATGTCAAGAGAC				
600 610 620 630 640 650 660 670				
CTTGTGGAGCTTGAACCAAGACCTGTGCGCATATAGAGTGGCCCCAAGAACATTAAGGTGAATCACTGCTAG				
1010 1020 1030 1040 1050 1060 1070				
GCTGTGGGTCTCACTAAGACATCTGCAATTGAGAGCTGGGCCCAAGACATCCGGGTAAACCTGGGTTC				

